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# Scientists as Teachers/ Communicators: The Importance of Biotechnology Education

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**S**hould researchers take an active role in helping to educate and inform the public about the use of advanced biotechnologies to improve food and fiber production systems? Given the gap between public understanding and public perception of biotechnology, genetic engineering or gene mapping, it's a question that more plant biologists, geneticists, and even breeders might consider asking themselves.

Biotechnology, " Frankenfood," genetic engineering, killer tomatoes, Jurassic Park. The public at large is presented with conflicting images of what scientists are doing, or will soon be doing, in labs across the country. Yet, for most Americans, the promise or threat of biotechnology remains in the realm of science fiction. Actual knowledge of what biotechnology or genetic engineering is remains extremely low (1).

As biofoods begin entering the marketplace in large numbers, the questions about biotechnology will move out of the labs and meeting rooms into the produce aisle, giving consumers the power to make choices about biotechnology-derived foods. With real products appearing on supermarket shelves, consumers will need objective information and educational opportunities to help them form individual opinions.

Why should researchers take an active role in educating and informing the public about the use of

biotechnology to improve food and fiber production systems? Public surveys (1,2) tend to indicate that university researchers are a highly trusted source of information related to biotechnology and genetic engineering. A 1992 survey (1) indicated that university professors, as a group, were one of the top three most credible sources of information about biotechnology, falling just behind dietitians/nutritionists and farmers/farm groups and just ahead of environmental groups.

If credibility with the public is not a problem, then why aren't more biotechnologists expounding on the potential of their research field? One problem often heard is that research scientists have too little time for such extracurricular activity. And if the time is available, how does one go about communicating to an audience where it is estimated that, on average, only 7 percent of the people will be scientifically literate?(3) Our advice to would-be communicators: go in well armed and with open eyes and an open mind.

### Whose language are we speaking anyway?

Researchers often wonder why the public understands so little about biotechnology and the molecular basis of life. Complicated phrases and complex subject matter, combined with a relatively low scientific literacy in this country, leave a wide chasm between the research community and a technology-wary public. If the public

at large and scientists could bridge that chasm, perhaps it would be appropriate to ask, "Why do we, as scientists and technology experts, understand so little about communicating with the public about biotechnology?"

To be effective educators and communicators, researchers must learn what it takes to translate their so-called Fudspeak – the language of Ph.D. biologists – into concepts and analogies that can be easily understood. Be willing to do as much listening as talking. Start with the familiar, and use what the audience knows to bring them to topics they want to learn more about. It often helps to start out by using a concept of biotechnology that is inclusive. If it is initially defined as applied recombinant DNA technology, most people will immediately feel disconnected from the subject matter.

To help define biotechnology on a scale that is familiar to everyone, it is often helpful to get an audience or class to come up with five things that begin with "F" that are from plants, animals, or microbes. With a bit of prompting, most crowds will likely be able to relate to FOOD, FIBER, FUEL, FEEDSTOCKS, and "F"ARMACEUTICALS. This opens up the discussion of how living organisms are used in our everyday lives. From this point it is often much easier to begin a discussion of how the modern tools of biotechnology (genome mapping, recombinant DNA) are being used in labs to improve and enhance the plants, animals, and microbes that we now depend on.

For example, when describing "genetic engineering" you can either launch into a descriptions of restric-

tion endonucleases and thermal cyclers (people in long johns on bicycles?), or you can compare DNA to a videotape. Both DNA and videotape are linear information tapes that carry encoded information that can be decoded,

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expressed, copied, spliced, and edited, and you can make copies of the edited versions.

Most people know what a radar detector is. Wouldn't it be nice to have a *biotechnology detector*

to help raise awareness? A little box that could fit on the dashboard, it would go off when the car goes by a place where biotechnology is used. Like a radar detector, the biotech detector could be adjusted for sensitivity. At the *classical* setting, any place that uses fermentations would set it off: a bakery, brewery, or a cheese plant. Adjust the sensitivity to *recombinant DNA* and you might have to drive past a university or company doing molecular biology research to set it off.

## Where do I go now? Assistance for scientists.

Not all scientists are in the teaching profession, but all scientists can teach by sharing their knowledge and expertise with others. Whether it's giving a presentation to students in your child's class on Career Day, serving as a mentor for an aspiring biologist, or talking to a local civic organization, being able to communicate effectively about your research and your scientific discipline is essential. Knowing

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where to find supporting education and communication materials on biotechnology can make the task that much easier.

## Resource guides to get you started and other good stuff

Resource guides are a quick way to track down supporting materials, people, and organizations that can provide assistance and know-how about biotechnology education and communication.

The **Biotechnology Education Resource Guide** from the University of Wisconsin is intended for teachers, 4-H leaders, extension agents, and anyone interested in obtaining materials or assistance in teaching biotechnology. It is updated regularly and is available from the University of Wisconsin Biotechnology Center (UWBC), 1710 University Avenue, Madison, WI 53705. The guide is also available at the UWBC gopher site at [calvin.wisc.edu](http://calvin.wisc.edu)

The Biotechnology Industry Organization (BIO) has produced a resource guide for educators entitled **Tools for Teaching Biotechnology: A Bibliography of Resources** (1994). Prepared by the BIO Education Committee, the guide provides pointers on appropriate books, compilations of lab exercises, videos, and other educational materials. Single copies of the guide are available from BIO, 1625 K Street, NW, Suite 1100, Washington, DC 20006-1604, Tel. (202) 857-0244.

## Science-by-Mail Program

### Making a connection with kids

If you would like to help students in the fourth through ninth grades understand more about your

particular scientific niche, or help redefine the scientist stereotype, the Science-by-Mail program may be of interest. This national pen-pal program has been pairing scientists with kids around the country for the past 8 years. Science activity packets are provided to children twice a year and encourage them to solve the science challenge with the advice and encouragement of their scientist pen-pals. Previous experience indicates the program benefits both student and scientist. Many of the local programs are run by non-profit Science-by-Mail chapters housed at 12 regional science museums. There is no cost to the scientist to participate and only a minimal fee for classroom use. For more information about becoming a scientist-by-mail, contact the Science-by-Mail National Office, Museum of Science, Science Park, Boston, MA 02114-1099, or call (800) 729-3300 or (617) 589-0437.

## Help from professional education associations - and even your own scientific society!

Just as plant molecular biologists and plant pathologists are brought together through their published journals and annual meetings, so too are biology educators represented by professional associations. The two largest such organizations are the National Science Teachers Association (NSTA) and the National Association of Biology Teachers (NABT). Biotechnology is often a focus of these associations' meetings and journal articles, as evidenced by the theme of NABT's 1994 annual meeting - "Biotechnology - A Gateway to the Future." The resources and materials provided by these organizations can

# Probe

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The official publication of the USDA Plant Genome Research Program. This newsletter is aimed at facilitating interaction throughout the plant genome mapping community and beyond.

Probe is a publication of the Plant Genome Data and Information Center, National Agricultural Library, ARS, USDA.

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## BIOTECHNOLOGY EDUCATION - SOCIETY CONTACTS

### National Association of Biology Teachers

11250 Roger Bacon Drive #19

Reston, VA 22090

Tel: (703) 471-1134

FAX: (703) 435-5582

*The American Biology Teacher*

### Science Education Network

Office of Education and Training

American Society of Microbiology

1325 Massachusetts Ave., N.W.

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Tel: (202) 942-9283

### Genetics Society of America

Administrative Office

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*GENerations* science education newsletter

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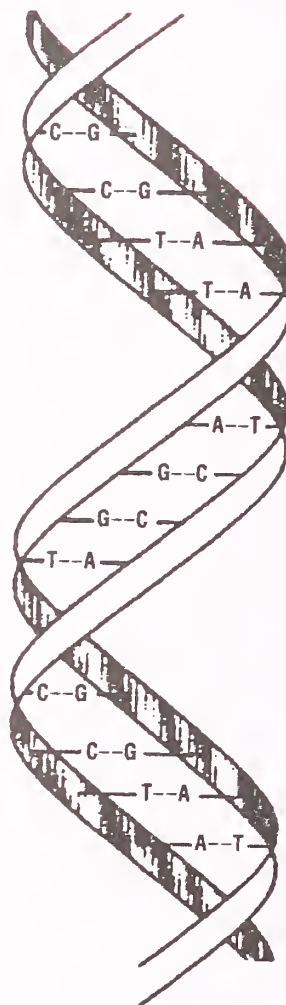
often provide guidance for bench scientists when talking to younger or less science-savvy audiences. In addition, many of the professional scientific societies (American Society of Plant Physiologists, American Society of Microbiology, etc.) have education committees or offices that will assist scientists in locating, developing, or preparing appropriate material for communicating.

Contact your professional society and see what it has – you might be surprised.

## On the net - education resources via the Internet

### GENTALK

This listserv was launched in August 1994 by Doug Lundberg at the Air Academy High School in Colorado Springs, CO. Gentalk was



created to serve as a forum for teachers, students, and other interested individuals concerned with genetic engineering and education. The discussions here tend to be aimed at students and teachers at the secondary school level. With a substantial amount of traffic, it's a good place to get a sense of the kinds of subjects that are being taught to students around the country. It provides a good opportunity to interact directly with students and teachers interested in genetic engineering from the comfort of your own office. To participate in discussions, send an e-mail message to: GENTALK@usa.net.

### PLANT-ED

The PLANT-EDUCATION newsgroup was created as a means for communication among instructors, lab preparators, and graduate assistants who teach courses in any aspect of plant biology including introductory botany, plant physiology, plant tissue culture, plant molecular biology, etc., at both the undergraduate and graduate levels.

This newsgroup serves as:

- A resource for the exchange of laboratory methods and classroom activities.
- A source of quick help for last-minute troubleshooting, conditions for plant growth, materials, and practical advice.
- A forum for discussing open-ended investigative laboratory projects.
- A forum for discussing textbooks.
- An archive of searchable information for future use by instructors of plant courses.

To subscribe, send an e-mail message to: biosci-server@net.bio.net Leave the "Subject:" line of the message blank



and enter the following line into the body of the message: "subscribe plant-ed"

## **BCEPP: The Biotechnology Education and Public Policy listserv (bcepp@relay.adp.wisc.edu)**

BCEPP (pronounced "bicep") is an Internet listserv used to post messages and exchange documents between education and public policy contacts at biotechnology centers, universities, governments, businesses, and other organizations. While the focus is not on teacher or student discussions, it provides an immediate, inexpensive, and infectious means of sharing information. Launched in December 1993, BCEPP has served as an excellent source of brief factsheets, press releases, contact information, and resource pointers on topics as they are unfolding. To subscribe, send a message to [listserv@relay.adp.wisc.edu](mailto:listserv@relay.adp.wisc.edu). In the body of the message, include the command "subscribe bcepp," followed by your name. Funded by a \$10 million grant from the biotechnology company Genetech, Access Excellence (AE) was launched in the summer of 1994 with 100 high school biology teachers across the country. According to Geoff Teeter of Genetech, "the goal of Access Excellence is to break down barriers so teachers can communicate with researchers and with other teachers."

The AE project is designed to improve high school biology education by:

- Linking teachers and scientists through an interactive computer network that provides peer support, as well as providing

## **OTHER GOOD PLACES TO LOOK ON THE INTERNET**

**Biotechnology Information Center gopher/WWW**  
[gopher inform.umd.edu:EdRes/Topic/AgrEnv/Biotech](http://gopher.inform.umd.edu:EdRes/Topic/AgrEnv/Biotech)  
<http://www.inform.umd.edu/EdRes/Topic/AgrEnv/Biotech>

**Biotechnology Education Home Page of Iowa State University**  
[http://www.public.iastate.edu/~biotech\\_ed\\_info/Biotech.html](http://www.public.iastate.edu/~biotech_ed_info/Biotech.html)  
 A collection of educational materials for ISU's Office of Biotechnology and other sources.

**Primer on Molecular Genetics**  
<http://www.gdb.org/Dan/DOE/intro.html>  
 A basic review of molecular biology/genome mapping from the Human Genome Program.

**MendelWeb Homepage**  
<http://www.netspace.org/MendelWeb/>  
 A resource for teachers and students regarding the origins of classical genetics, data analysis, basic plant science, and the history and literature of science.

access to critical sources of new information about leading-edge research and developments in the biological sciences. The program currently operates on the commercial network America Online (see keyword Excellence), and has recently been made available via the World Wide Web (WWW). Point your WWW browser to <http://www.gene.com/ae/>

- Supporting teachers and scientists in the development of strategies and resources to communicate this knowledge to students, educators, policymakers, and the public.
- Creating partnerships between teachers and scientists in implementing the national science education reform agendas locally and regionally.

Access Excellence also functions as a news service and as a

library. "Teachers can keep up to date on the latest news in biotechnology research and education," notes Teeter. The AE project also facilitates access to teaching materials and databases.

## **Literature Cited**

1. Hoban, T.J. and P.A. Kendall. 1992. Consumer Attitudes about the Use of Biotechnology in Agriculture and Food Production. (Project report #91-EXCA-3-0155) North Carolina State University, Raleigh, NC.
2. Rothenberg, L. 1994. Biotechnology's issue of public credibility. *Trends in Biotechnology* 12:435-438.
3. Hassler, S. 1994. Biotech's role in science education. *Bio/Technology* 12:647. ♦

Mention of a trade name or brand does not constitute endorsement or recommendation by the Department over similar products not named.

Touching Base with Clare Nelson



# SolGenes, an ACeDB Database for the Solanaceae

Clare Nelson, Database Curator  
Department of Plant Breeding and Biometry  
Cornell University

**S**olGenes, along with GrainGenes and RiceGenes, is one of three plant genome databases under development at Cornell University. All three are based on the ACeDB software and funded by the USDA, Plant Genome Project.

The scope of SolGenes is the solanaceous crop species – to date including tomato (*Lycopersicon* spp.), potato (*Solanum* spp.), pepper (*Capsicum* spp.), and their wild relatives. Genomic research data from other *Solanum* species (such as *S. melongena*, eggplant) and other genera in the family (*Datura*, *Petunia*, and *Nicotiana*, for example) are not yet featured but are also welcome.

The core of SolGenes consists of genetic maps of the various species, stored and displayed in ways that allow for ready cross-referencing. Currently, available are tomato, potato, and pepper RFLP maps constructed at Cornell, as well as a tomato morphological map assembled by S.D. Tanksley with many refinements on chromosomes 3 and 6 added by M. Koornneef and colleagues. We are adding potato maps from C. Gebhardt (Max-

Planck-Institut) and Dutch colleagues, and new pepper maps from M. Kyle at Cornell and from French researchers. Since all these maps share at least some probes, their availability in a single database should ease the construction of useful consensus maps for these crop species.

Also available is a recently updated list of more than 3,000 tomato germplasm stocks (mutants, chromosome testers, etc.) with passport information, maintained at the Tomato Genetic Resources Center (TGRC) in Davis, CA, by R. Chetelat. Work in generating images of these plants and loading them into the database is in progress. Recently, a set of 50 *L. pennellii* single-segment introgressions into a *L. esculentum* background was constructed by Y. Eshed and characterized with some 350 RFLP and isozyme markers. These lines are available from the TGRC, and the marker data defining the introgressed regions were contributed to SolGenes. ACeDB databases are equipped with routines to display chromosomal regions, and these work nicely for the introgressed segments.

These entries are connected

and cross-referenced by a background of literature citations (130), a colleague directory (541), catalogs of probes (1,000), loci (2,000), and restriction enzymes (340). Lacking are physical-mapping data, and we will be seeking YAC and BAC information, primer sequences, probe sequences, and related information. Increasingly relevant are gene-mapping and variety-discrimination studies with molecular markers, and we have (and seek) sources of such data for all three major species.

Also of interest is the increasing application of molecular information to breeding, and results in this area will be incorporated; that is, field studies or marker-assisted selection results.

Another kind of information that might be welcomed by breeders and researchers is more germplasm catalogs. We will not try to incorporate existing catalogs, but where germplasm databases are already accessible, SolGenes might be able to direct users to them.

The entire database may be obtained via anonymous ftp from [probe.nalusda.gov:pub/solgenes](http://probe.nalusda.gov:pub/solgenes), if you wish to set it up on a local (typically Unix-based) computer.



There is a Macintosh version of ACeDB called MacAce, but to date no one (me, in other words) has compiled the SolGenes data into it. You can access SolGenes via a text interface through either of these gopher servers:

nightshade.cit.cornell.edu port 71  
probe.nalusda.gov port 7006

The URL for access to SolGenes via the World Wide Web is:

<http://probe.nalusda.gov:8300>

The text-based ways of accessing the database do not take full advantage of the graphical displays available with a version running locally, though all the data, including images in TIFF format, are still available. An X-window emula-

tor program, however, running on your local PC or Macintosh (MacX, for example) will give you, via remote logon, the full range of graphical displays built into ACeDB databases.

If you would like to contribute information to SolGenes, we would like to hear from you. Data need not be in a special format; our group can do most of the preparation. We also invite suggestions for sources of data and suggestions about data types that would be of use to you, as well as ways in which you would prefer to view or search the database. ACeDB databases, while they have some underlying structure, leave a curator free to adapt data interconnections to users' preferences.

A mailing list of interested users is maintained and messages may be posted by any subscriber to the rest of the group via e-mail to [solfolk@nightshade.cit.cornell.edu](mailto:solfolk@nightshade.cit.cornell.edu). To be placed on or taken off this list, send an e-mail message to me at the address above or to [cnelson@nightshade.cit.cornell.edu](mailto:cnelson@nightshade.cit.cornell.edu).

Several scientists in the United States and Europe have agreed to serve on an informal steering committee for SolGenes. They will provide consultation about the direction of development and assist as liaisons with other workers in the solanaceous crops who might want to use and/or contribute data to the database. Please feel free to communicate with them in this capacity. ♦

## Steering Committee

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## Congratulations

### Plant Genome Researchers Elected to National Academy of Sciences

**I**n recognition of their continuing achievements in original research, two active contributors to the USDA Plant Genome Research Program, in April, were elected to membership in the National Academy of Sciences. Congratulations to Steven D. Tanksley, Liberty Hyde Bailey Professor of Plant Breeding at Cornell University (Ithaca, NY); and Ronald R. Sederoff, Professor, North Caro-

lina State University Department of Forestry (Raleigh), for attaining one of the scientific community's highest honors.

Also among the distinguished plant researchers elected to the Academy are Bob B. Buchanan, Professor, Department of Plant Biology, University of California, Berkeley; and Elliot M. Meyerowitz, professor, division of biology, California Institute of Technology, Pasadena.

The National Academy of Sciences is a private organization of scientists and engineers dedicated to the furtherance of science and its use for the general welfare. It was established in 1863 by a congressional act of incorporation, signed by Abraham Lincoln, that calls on the Academy to act as an adviser to the Federal Government, on request, in any matter of science or technology. The total number of current active members is 1,733. ♦

### Plant Genome Researchers Among Academy's Honored Members

Several distinguished National Academy of Sciences members have been involved with plant genome research. The Plant Genome Research Program wishes to commend these individuals for the significant contributions to scientific understanding and their receipt of one of the science community's highest honors. Listed below with their institutions, they include:

Frederick M. Ausubel  
Harvard University

Lawrence Bogorad  
Harvard University

Winslow R. Briggs  
Carnegie Institution of Washington

Andre T. Jagendorf  
Cornell University

S. J. Peloquin  
University of Wisconsin

Ronald L. Phillips  
University of Minnesota

Charles M. Rick  
University of California, Davis



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## Off the Wire



# New Plant Genome Information—Online!

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Plant Genome Data and Information Center  
National Agricultural Library, ARS, USDA  
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Today, more than ever, information is your key to success. If you are planning research projects; looking for collaborators, research techniques, and tools; or interested in reporting your research progress, educating students, and developing markets, visit the Plant Genome Data and Information Center (PGDIC) — using your computer and modem.

PGDIC's online information resource provides up-to-date information on current research, grants, plant DNA libraries, plant genome events and short courses, personal contacts, *PROBE* articles, and more. Described below are some of its exciting features and directions for plugging in.

### Plant Genome Grant Information

Plant Genome grants awarded since the program's inception are currently listed by year. Each entry includes the name of the principal investigator, institution, title of the proposal, and a CRIS (Current Research Information Service) accession number. In the near future, the World Wide Web (WWW) file format will provide active links to the original full text CRIS record.

A new bibliography has been compiled from the 1991 Plant Genome Grants. It features a selection of the most significant papers published from these grants. PGDIC will update it and compile additional bibliographies on a regular basis.

### Calendar of events

Timely listings of important national and international meetings, conferences, and workshops are posted monthly. Listings include event title, location and dates, contact information, and more. Also listed are short courses to refresh and build skills.

### Plant Genome Phonebook

The Plant Genome Phonebook lists contact information for developers and other individuals working on the plant genome databases. The Phonebook lists names, addresses, telephone and fax numbers, and e-mail addresses, along with a brief description of the individual's role in the program.

### Plant DNA Library Files

By popular request, PGDIC's online resource features Plant DNA Library Files, which contain information of interest to researchers, educators, and the business commu-

nity. Data were collected either by direct author submission or by careful reading of the recent research literature.

Whenever possible, the files contain information about the nature of the library (genomic, cDNA, YAC); nucleic acid preparation methods; cloning vectors used; cloning site; insert size; estimated titers; how the library was screened; clones isolated, including their GenBank/EMBL/DDBJ accession numbers; the citation reference; contact person(s) and availability. Coming soon is a form to facilitate direct author submission. We encourage all researchers to participate in developing this valuable resource.

### Plant Genome Mapping Projects

The plant genome mapping project files have many uses. For example, grant proposal preparation is greatly aided when you know which projects have been funded. The information in these files will enable you to develop unique proposals that attract funding. Also, today's complex cross-cutting research is highly dependent on collaboration, and the projects directory will help you find colleagues with similar interests. In addition, students looking for graduate and postdoctoral research can use these files to locate suitable laboratories.



The files were created by searching the databases CRIS/ICAR (USDA and CARC, North America), SPAAR (World Bank, USA), ARRIP (CSIRO, Australia), and AGREP (European Community Agriculture Research) using the AGRISEARCH Silver Platter CD-ROM. The files are updated annually. (See the sidebar on new plant genome mapping projects in this issue.)

The sponsored research projects on plant genome mapping were found by using names of plant species and the following terms: gene map, genetic mapping, gene mapping, genetic map, genome map, genome mapping, linkage map, linkage mapping, physical map, physical mapping, RFLP mapping, RFLP map, molecular map, molecular mapping, chromosome map, chromosome mapping, and quantitative trait loci.

### Probe

*Probe*, the official newsletter of the USDA Plant Genome Research Program, is now available online. All issues are accessible via gopher. The two most recent issues are also available as hypertext documents on the WWW. Retrospective conversion of the earlier issues to HTML for the WWW is under way.

You have two options for downloading *Probe* articles from gopher. Separate gopher files have been created for individual articles; this allows you to select individual articles without having to download an entire issue. Should you choose to download an entire issue, PGDIC has also provided a separate file with complete issues.

### Much more...

At present, PGDIC's online resource contains practical information about the Plant Genome Research Pro-

gram; research techniques and resources, including molecular markers; patents; germplasm; and much more. We invite you to mine these valuable information resources via gopher and WWW.

### Access

To access the (online resource) via gopher:

Point your gopher to:

• [gopher.nalusda.gov](mailto:gopher.nalusda.gov)

Select Information Centers, then select Plant Genome Data and Information Center

WWW access: The URL is

• [http://www.nalusda.gov/answers/info\\_centers/pgdic/pgdic.html](http://www.nalusda.gov/answers/info_centers/pgdic/pgdic.html)

Please direct your questions about PGDIC's online information resource to the Plant Genome Data and Information Center, (301) 504-6613. ♦

## New Plant Genome Mapping Projects Increase in Number, Scope

Andrew Kalinski

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The number of sponsored research projects and plant species used for genome mapping increased significantly during 1994. A search of the AGRISEARCH Silver Platter CD-ROM (September 1994) shows the trends in North America (USA and Canada) and Europe.

In North America, such additional plant species as spruce, magnolia, cocoa, celery, and papaya have been used for genome mapping during the last year. European genome mapping projects have

focused on pea, peach, mushroom, rye, cucumber, corn, liliun, grass, fungi, and wheat.

The table below shows the increase in the number of genome mapping projects between the years 1993 and 1994. ♦

Table 1.

	1993	1994
North America	214	462
Europe	26	70
Australia	13	11
Total	253	543



United States  
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SUSAN McCARTHY  
Editor



National Agricultural Library

## Survey of *Probe* Readers

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| <input type="checkbox"/> other _____            |  |

Please , describe your specific position: \_\_\_\_\_

### Do you have access to the Internet? Yes ☐ No ☐

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### What platform do you use? Please check all that apply.

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### Have you viewed the Plant Genome Database(s)? Yes ☐ No ☐

#### If yes, have you found information in the Plant Genome Database(s)?

Yes ☐ No ☐

If no, why not (ie, do not know how to access the database(s)) \_\_\_\_\_

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- ☐ Share the information with others. How many? \_\_\_\_\_
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1 = extremely 2 = very 3 = somewhat 4 = slightly 5 = not at all

Section	Relevance	Usefulness	Thoroughness
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2. Database updates and reports	[ ]	[ ]	[ ]
3. Experimental concepts	[ ]	[ ]	[ ]
4. Stock center and germplasm	[ ]	[ ]	[ ]
5. Calendar of events	[ ]	[ ]	[ ]
6. Internet resources	[ ]	[ ]	[ ]
7. Other genome programs	[ ]	[ ]	[ ]
8. Commercialization issues	[ ]	[ ]	[ ]
9. Introducing program personnel	[ ]	[ ]	[ ]
10. General Interest articles	[ ]	[ ]	[ ]

Which of the above listed topics would you like to see receive more coverage? Please check all that apply.

1 [ ] 2 [ ] 3 [ ] 4 [ ] 5 [ ] 6 [ ] 7 [ ] 8 [ ] 9 [ ] 10 [ ]

How could the sections above be improved to better suit your needs? Please, indicate section number to which recommendation(s) refer. \_\_\_\_\_

\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

Do you have an idea for an article? *Topic:* \_\_\_\_\_

\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

We estimate that it will take you between 20-30 minutes to complete this survey. Send comments regarding this burden to Department of Agriculture, Clearance Officer, OIRM, AG BOX 7630, Washington, DC 20250-7630. Thanks in advance for your help. Please fold, tape, and mail (or fax) completed survey by October 15, 1995 to: PDGIC Customer Survey, USDA, ARS, National Agricultural Library, 4th Floor, 10301 Baltimore Blvd., Beltsville, MD 20705-2351. FAX (301) 504-7098

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## Taking Stock



# Bacterial Artificial Chromosome Libraries for Genome Analysis

Guo-Liang Wang, and Pamela C. Ronald

Department of Plant Pathology  
University of California at Davis  
Davis, CA

One of the essentials for the success of map-based cloning and physical analysis of large chromosomal regions is the availability of libraries containing large inserts of genomic DNA. In recent years, yeast artificial chromosome (YAC) libraries have been constructed for human (Burke et al. 1987), mouse (Chartier et al. 1992), and plant species, such as *Arabidopsis* (Ward and Jen 1990, Grill and Somerville 1991), tomato (Martin et al. 1992), maize (Edwards et al. 1992), barley (Kleine et al. 1993), and japonica rice (Umehara et al. 1994).

These libraries have made valuable contributions to the production of physical maps of large regions and the isolation of many important genes (Arondel et al. 1992, Giraudat et al. 1992, Martin et al. 1994, Leyser et al. 1993). However, the large percentage of chimaeric (Green et al. 1991, Libert et al. 1993, Umehara et al. 1994) and unstable (Neil et al. 1990, Dunford et al. 1993, Schmidt et al. 1994) YAC clones has hindered the usefulness of these libraries. Difficulties in isolation of YAC insert DNA and low transformation efficiency also affect YAC library construction.

Bacterial artificial chromosome (BAC) libraries overcome many of the disadvantages of YAC libraries (Shizuya et al. 1992). This system uses an F-factor-based vector and is capable of maintaining human genomic DNA fragments of > 300 kb. Compared with YAC cloning, DNA can be cloned with high efficiency, easily manipulated, and stably maintained in *E. coli* (Shizuya et al. 1992). Recently, BAC libraries have been constructed for *Arabidopsis*, sorghum and rice (Wang et al., unpublished; Woo et al. 1994; Wang et al. 1995). All clones tested from the rice and sorghum BAC libraries hybridized to a single chromosomal location using fluorescence *in situ* hybridization (FISH) analysis (Jiang et al. 1995; Woo et al. 1994). These results indicate a very low level of chimerism in these libraries.

Plant BAC libraries have been used successfully in several collaborative efforts. For example, BAC clones linked to disease resistance genes have been isolated from the *Arabidopsis* and rice libraries (6x and 3x genome equivalents, respectively) (Wang et al., unpublished; Wang et al. 1995). In addition to

their use for gene isolation within a species, BAC libraries from species with small genomes can be used to identify syntenous chromosomal regions in plant species with larger genomes. For example, compared with rice, other cereal crops such as maize, wheat, barley, and rye have a much higher percentage of repetitive sequences, yet the gene order is highly conserved along the chromosomes.

To test the usefulness of the BAC library in intergenomic gene cloning, we have isolated clones from the rice BAC library corresponding to a region of the barley genome containing the disease-resistance gene, *Rpg1* (Kilian et al., unpublished). Single-copy end-probes of rice BAC clones can be used to jump or walk between genes in barley to avoid repetitive sequences. Finally, BAC clones can be mapped in plant chromosomes by FISH analysis (Jiang et al. 1995). This technique can be used for rapid determination of the chromosomal location of genomic clones or the physical distance between genetically mapped clones. Since BAC libraries can be constructed in a short time and analyzed more



efficiently than can YAC libraries, the BAC system is likely to become an important tool for plant genome analysis.

The rice and *Arabidopsis* BAC libraries are available for distribution. Interested researchers should send requests to Pamela Ronald, pcronald@ucdavis.edu, phone: (916) 752-1654 or fax (916) 752-5674.

This project was supported by grants from the Rockefeller Foundation and USDA (NRICGP, # 9300834).

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## Probe Note

Dear Readers:

Your interests are important to us. Articles and news items are welcome.

Editor

## Plant Chromosomes at High Resolution

Regina Martin, Gerhard Wanner, and Reinhold G. Herrmann  
Botanisches Institut der Ludwig-Maximilians-Universität,  
Menzinger Straße 67  
D-80638 München, Germany

**T**he past two decades have seen enormous progress towards understanding eukaryotic genes and genomes. Recombinant DNA technology has provided this power and hardly any contemporary experiment of gene structure and function is done today without recourse to methods of molecular biology. Considerable detail is known of the fine structure of genes and regulatory proteins that control

not only single metabolic steps but even complicated developmental processes.

It became obvious, however, that a gene can no longer be por-

electron microscopy (FESEM) provides a powerful tool for studying such ultrastructural detail. The resolution of the instrument is in the order of 1-2 nm, and the detection of fibrillar structures in chromo-

somes of less than 10 nm corresponding to the elementary fiber has recently

become possible. An optimized preparation technique allows the production of a high number of spreads of surface-exposed chromosomes that are appropriate for examination of chromosomal fine structure at the different stages of

### Developments

trayed only one-dimensionally and that an understanding of the dimensions between the macromolecule DNA and the cytological entity *chromosome*, with its periodically recurring conformational changes, will be required. Yet the relationships between topographical, physical, and genetic distances of genes and their impact on genetic events, gene expression, and evolution have largely escaped analysis.

It is therefore desirable to unravel chromosome structure and gene arrangement at the ultrastructural level. Modern high-resolution field emission scanning



Figure 1 a: Electron micrograph of anaphase chromosomes of barley (*Hordeum vulgare*), cv. Marinka.

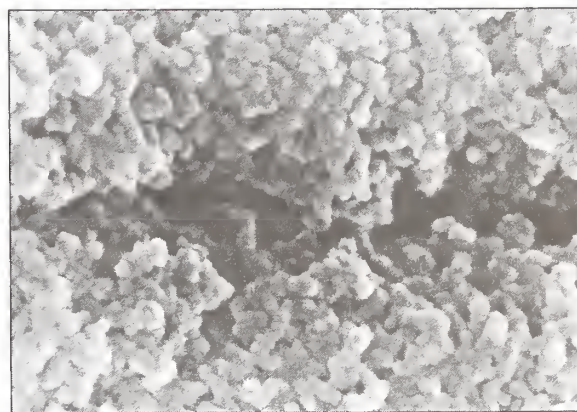


Figure 1 b: Surface structure of an anaphase chromosome of barley. Magnification 10 x figure 1 a.





Figure 2 a: Electron micrograph of prophase chromosomes of barley, cv. Marinka.

fibers of about 30 nm (fig. 1). Because of the high compaction of chromatin fibers, it is impossible to detect the basic chromatin organi-

zation at this stage. More detail can be seen in condensing or decondensing chromosomes (fig. 2), for instance, in prophase chromosomes that exhibit a less compact fiber arrangement. Furthermore, *in situ* hybridization by signal detection of gold-labeled probes in chromosomes with a relatively low degree of condensation in the FESEM may aid in unravel-

ing the unknown detail of sequence (gene) arrangement as well as the higher three-dimensional order of chromatin fibers. ♦

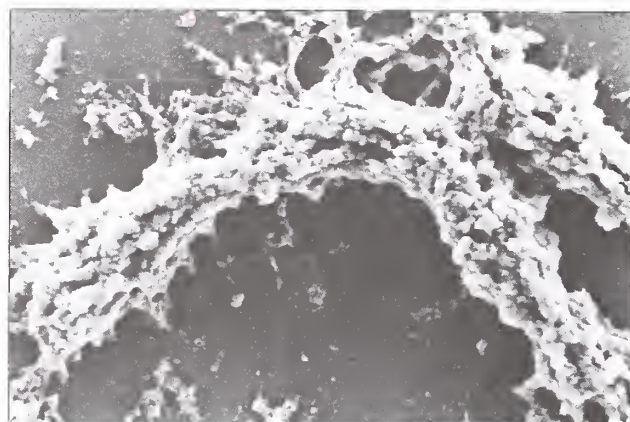


Figure 2 b: Telomeric region of a prophase chromosome from (a). Magnification 5 x figure 2 a.

the cell cycle (Martin et al., Chromosome Res. 2: 411-415, 1994).

Metaphase and anaphase chromosomes are characterized by a highly compact structure of chromatin. High resolution shows a smooth surface and a preponderance of

## FYI

# Announcing the Journal of Quantitative Trait Loci

Dr. Patrick Byrne  
Department of Agronomy  
University of Missouri  
Columbia, MO

**T**he Journal of Quantitative Trait Loci (JQTL), sponsored by the Crop Science Society of America (CSSA), will provide a peer-reviewed, fully electronic forum in which articles dealing with the theory and practice of QTL analysis will be published.

The publication format will facilitate links to related publica-

tions and databases and will permit the inclusion of more complete analyses than are generally feasible in bound media. Improved publication speed, easy and inexpensive access, and flexibility should make JQTL a preferred journal for the publication of papers dealing with the analysis of inheritance of quantitative traits.

## Purposes of the Journal

1. JQTL will publish articles relevant to the analysis, manipulation, and use of genes modifying quantitative characters in any species. We are defining quantitative characters as those for which the phenotypic variation among genotypes is continuous and cannot be separated into discrete classes. This definition of QTL makes no assumptions regarding the number of genes controlling such characters, nor the magnitude of genetic effects. When appropriate, authors will be encouraged to include data sets on which





their analyses depend.

2. JQTL will serve as a medium for announcing, describing, and storing new software developed for QTL analysis.

3. JQTL will publish secondary analyses of primary data sets when such analyses prove novel and illuminating.

4. JQTL will publish worthy editorial commentaries and review articles as space and interest warrant.

## General Standards

Papers will be submitted via either electronic transmission or on diskette. They will consist of ASCII text, with .gif files holding images. Papers will be written in general accordance with style standards of Crop Science (Publications Handbook and Style Manual, 1988, American Society of Agronomy (ASA), Madison, WI). Papers will be submitted to the editor, who will then request review by two technical editors.

## Information To Be Included in Articles Submitted

All articles should contain (a) title; (b) affiliation, phone number, and e-mail addresses of all authors; (c) abstract briefly summarizing the work; (d) introduction, methods, results and discussion sections in accordance with ASA guidelines; and (e) literature cited.

For all articles containing data sets, authors must supply a data dictionary (description of data fields) and a description of how the data were gathered.

Software submission: All software described in a JQTL article should be, if at all possible, available for JQTL readers. Ideally, an anonymous ftp site would already exist

from which software could be downloaded. If this is not the case, and the software was developed by the authors, then the software should be uploaded to [hordeum.oscs.montana.edu](http://hordeum.oscs.montana.edu). All executable software should be accompanied by source code, if available, as well as a user manual. Acceptable formats are:

- Unix: a compressed tar file (compressed with either the compress program or by gzip)
- DOS/Windows: a PKZIP (.zip) file
- Macintosh: a StuffIt archive (.sit) file

## Originality and Novelty

To be considered for publication, neither data nor analyses should have been published previously in any peer-reviewed journal, book, or bulletin. While updates (that is, second year data sets or data sets gathered in new environments using lines already characterized) may be considered for publication, they will generally be accepted as appendices to previous articles. New analyses of previously published data sets will be accepted if they provide novel insights into the data.

## Peer Review and Comments

Each submitted article will be reviewed by two scientists familiar with the area of research. They will be asked to review the manuscript for compliance with the above criteria, to judge suitability of the article for inclusion in JQTL, and to write brief critiques of the manuscript to be returned to the author. The editors will attempt to evaluate the performance of submitted software.

## Submission Protocol

Articles may consist of text, tables, and data sets (all in ASCII format) and figures (in .GIF format). Other acceptable formats may be announced in the future. There are no size limitations.

Before submission, authors should e-mail the editor (current address: [blake@hordeum.oscs.montana.edu](mailto:blake@hordeum.oscs.montana.edu)) to request a submission number. Files should then be renamed to include the submission number (for example, text##.asc, fig1##.gif, fig2##.gif, tabl##.asc, data##.asc). This should prevent one submission overwriting another.

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headquarters for HTML formatting and finally to the USDA, ARS, National Agricultural Library for immediate publication. JQTL will be continuously updated with new articles.

### Journal Access

On April 1, 1995, JQTL became available for public online access

from the National Agricultural Library via World Wide Web at <http://probe.nalusda.gov:8000/> under the heading "Newsletters, Journals, and Other Publications."

No charge will be levied for publication or for journal access during 1995, although nominal fees may be assessed at a later date.

JQTL will be indexed in the

AGRICOLA bibliographic database and by other biological indexing services.

### Journal Annual

By the end of the first year of publication, we hope to have the capacity to make annual CD's of the journal available for a nominal fee.

## Introducing... Dr. Steven D. Tanksley

Steven D. Tanksley's recent election to the National Academy of Sciences (see related story in this issue) caps a career studded with activity and achievement.

Tanksley is the Liberty Hyde Bailey Professor of Plant Breeding at Cornell University, Ithaca, NY, a position he has held since last year. He also is principal investigator for the Solgenes database, which contains mapping and related information for the *Solanaceae* – tomato, potato,

eggplant, and bell pepper.

In 1993, Tanksley was among a team of Cornell scientists who successfully cloned the first gene for disease resistance in tomato, using a technique known as map-based cloning developed for the Human Genome Project. This research opened the possibility of cloning similar resistance genes in other plant species.

Tanksley joined Cornell's faculty in 1985 as an associate professor, and became a professor

of plant breeding in 1991. Before coming to Cornell, he was an assistant professor at New Mexico State University, Las Cruces, since 1981. In 1979, he was a postdoctoral fellow at the University of California-Davis, where he earned his doctorate in genetics.

Tanksley earned his bachelor's degree in agronomy from Colorado State University in 1976. He is a native of Hattiesburg, Mississippi. ♦

## Calendar



# Calendar of Upcoming Genome Events

## MEETINGS

October 1-4: Engineering Plants for Commercial Products/Applications, Lexington, KY. Contact: International Symposium on Engineering Plants, c/o Conferences and Institutes, 218 Peterson Service Bldg., Lexington, KY 40506-0005. VOICE: (606) 257-3929, FAX: (606) 323-1053, EMAIL: monica.stoch@ukwang.uky.edu

October 16-20: Third International Rice Genetics Symposium, IRRI, Philippines. Contact: Dr. G.S. Khush, International Rice Research Institute, P.O. Box 933, Manila, Philippines.

October 19-20: Biotechnology Colloquium as part of the North American Plant Protection Organization Annual Meeting, October 16-20, 1995, Saskatoon, Canada. Contact: Jane Thibert, Program Manager, Plant Protection Div., Agriculture and Agri-Food Canada, Food Production & Inspection Br., 59 Camelot Dr., Nepean, Ontario, Canada K1A 0Y9. VOICE: (613) 952-8000, FAX: (613) 952-0809.

October 22-25: Third New Crops Symposium, Indianapolis, IN. Contact: Jules Janick, Indiana Center for New Crops and Plant Products, Purdue University, 1165 Horticulture Bldg., West Lafayette, IN 47907-1165. FAX: (317) 494-0391.

November 6-10: International Cactus Conference: 6th National and 4th International Conference about the Knowledge and Utilization of Cactus Pear (*Opuntia spp*) and Other Cacti with Economic Value, Guadalajara, MEXICO. Contact: Erick de la Barrera Montpellier. EMAIL: ebarrera@udgserv.cencar.udg.mx. ASCII file available at: anonymous@udgftp.staff.udg.mx (file is /pub/opuntia.txt)

November 16-18: American Association for Clinical Chemistry 1995 San Diego Conference: Nucleic Acids: A Decade of Discovery, San Diego, CA. Contact: American Association for Clinical Chemistry, 2101 L St. NW, Suite 202, Washington, DC 20037. VOICE: (800) 892-1400 or (202) 857-0717; FAX: (202) 833-4576.

December 9-13: American Society for Cell Biology 35th Annual Meeting, Washington, DC. Contact: American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD 20814-3992. VOICE: (301) 530-7153, FAX: (301) 530-7139, EMAIL: ascbinfo@ascb.faseb.org.

January 3-6, 1996: Pacific Symposium on Biocomputing, Kohala Coast, HI. Contact: Sharon Surles, PSB Conference Coordinator, IS, Inc., Suite 203, 5330 Carroll Canyon Rd., San Diego, CA 92121. VOICE: (619) 658-9782, FAX: (619) 658-9463, EMAIL: psb@intsim.com.

June 17-23, 1996: 4th International Technical Conference on Plant Genetic Resources, Leipzig, Germany. Contact: Dr. Cary Fowler, Food and Agricultural Organization, Via delle Terme di Caracalla, 00100 Rome, Italy. VOICE: 39-6-5225-5925, FAX: 39-6-5225-5271, EMAIL: cary.fowler@fao.org.

July 21-24, 1996: International Fructan Symposium, Logan, UT. Contact: N. Jerry Chatterton, USDA-ARS, Forage and Range Research, Utah State University, Logan, UT 84322-6300. VOICE: (801) 797-2249, FAX: (801) 797-3075, EMAIL: njchatt@cc.usu.edu

## WORKSHOPS AND COURSES

October 8-17: Istituto di Ricerche di Biologia Practical Course: Frontiers of Protein Structure Prediction, Pomezia, Rome, Italy. Contact: Ms. Tiziana Gobbi, IRBM, Via Pontina Km 30.600, I-00040 Pomezia, Rome, Italy. VOICE: +30 6 91093201, FAX: +39 6 91093654, EMAIL: gobbi@irbm.it, WWW: <http://www.mrc-cpe.cam.ac.uk/predict/>

October 13-14: Workshop on Gene-Finding and Gene Structure Prediction, Philadelphia, PA. Contact: David Searls, Dept. of Genetics, CRB475, University of Pennsylvania School of Medicine, 422 Curie Blvd., Philadelphia, PA 19104-6145. VOICE: (215) 573-3107, FAX: (215) 573-3111, EMAIL: dsearls@cbil.humgen.upenn.edu.



October 23-26: **Recombinant DNA Methodology and DNA Sequencing**, Lake Tahoe, NV. Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620 Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

October 23-26: **Polymerase Chain Reaction Techniques and DNA Sequencing**, Lake Tahoe, NV. Contact: Director, Center for Advanced Training in Cell and Molecular Biology, Catholic University of America, 620

Michigan Ave., NE, Washington, DC 20064. VOICE: (202) 319-6161, FAX: (202) 319-4467, EMAIL: millerm@cua.edu.

November 8-21: **Molecular Markers for Plant Breeding & Plant Genetics**, Cold Spring Harbor, NY. Contact: Cold Spring Harbor Laboratory, The Meetings Office, 1 Bungtown Road, P.O. Box 100, Cold Spring Harbor, NY 11724-2213. VOICE: (516) 367-8346, FAX: (516) 367-8845, EMAIL: meetings@cshl.org

## Do You Know About the NRI AREA and Strengthening Programs?

**Postdoctoral Fellowships** are available for U.S. citizens graduating January 1, 1993, through June 15, 1996. Research must pertain to and proposals be submitted to one of the program areas described in the NRI Program Description.

**New Investigator Awards** are available to investigators beginning their career-track research careers. Research must pertain to and proposals be submitted to one of the program areas described in the NRI Program Description. Applicants may not have received competitively awarded Federal research funds beyond the level of pre- or post-doctoral research awards.

**Standard Strengthening Research Project Awards** are available to faculty with full-time appointments at USDA-EPSCoR State<sup>1</sup> institutions or small- and mid-sized institutions with limited institutional success<sup>2,3</sup> and who have not received a USDA NRICGP competitive grant within the past 5 years. Research must pertain to and proposals be submitted to one of the program areas described in the NRI Program Description.

**Research Career Enhancement Awards** (for sabbatical leave) are available to faculty at small- and mid-sized institutions with limited institutional success<sup>2,3</sup> or USDA-EPSCoR State<sup>1</sup> institutions and who have not received a USDA NRICGP competitive grant within the past 5 years.

**Seed Grants** are available to provide funds to

enable investigators at small- and mid-sized institutions with limited institutional success<sup>2,3</sup> or USDA-EPSCoR State institutions (and who have not received a USDA NRICGP competitive grant within the past 5 years) to collect preliminary data in preparation for applying for a standard research project grant.

**Equipment Grants** are available to any degree-granting institution that has had limited success.<sup>3</sup> Matching funds are required with a maximum equipment cost of \$100,000. Although the principal investigator is to be the principal user of the requested equipment, arrangements for sharing equipment among faculty are encouraged.

Contact the NRI office (telephone (202) 401-5022) your Program Directory, or check the 1996 Program Description for further information. ♦



<sup>1</sup>USDA-EPSCoR States (Experimental Program for Stimulating Competitive Research) means States that have had a funding level from the USDA NRICGP no higher than the 38th percentile of all States, based on a three-year rolling average. In addition, all U.S. territories and possessions qualify as USDA-EPSCoR states.

<sup>2</sup>Small- and mid-sized institutions means academic institutions with a total enrollment of 15,000 or less.

<sup>3</sup>Limited institutional success means institutions that are not among the top 100 universities and colleges for receiving Federal funds for science and engineering research as listed in the most recent release of Selected Data on Federal Support to Universities and Colleges (National Science Foundation).

## Announcing

The International Plant Genome IV Conference

**January 14-18, 1996**

Town & Country Hotel • San Diego, CA



### SCIENTIFIC PROGRAM

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- USDA, NRI Competitive Grants Office

#### CHAIRPERSONS

- S. Heller, USDA/ARS, Beltsville MD
- J. Mksche, USDA/ARS, Beltsville, MD
- M. Gale, John Innes Centre, Norwich, UK
- S. McCouch, IRR, Philippines

Participants are invited to submit abstracts for the poster session. Abstract Deadline is November 1, 1995.

#### SUNDAY, JANUARY 14

##### Workshop

JAMES IRVINE, Texas A&M University  
International Consortium for Sugar Cane Biotechnology

##### Workshop

DAVID NEALE, USDA Forest Service  
Forest Tree Genome Part 1 & 2

##### Workshops

Maize: Mike McMullen  
Rice: Susan McCouch/Nori Kurata/  
Guo-Fan Hong/Eun  
Cotton: Andy Paterson  
Arabidopsis: Caroline Dean  
Soybeans/Legumes: Randy Shoemaker  
**Welcome Reception**

#### MONDAY, JANUARY 15

##### Continental Breakfast

##### Welcome Address

STEPHEN HELLER, USDA/ARS

##### Session 1 - Technology

Chairperson LELAND ELLIS, TAMU

##### Plenary Lecture -

MICHAEL LOVETT, Univ. of Texas  
RADOJE DRMANAC, Hyseq Inc. -  
Mutation Screening and DNA  
Sequencing by the First Generation  
Super Chips  
JOHN ARMOUR,

##### Posters (odd #'s), Exhibits & Computer Demos - Coffee/Soda

##### Session 2 - Genomes and Diversity

Chairperson GARY MCCONE, USDA

##### Plenary Lecture -

STEPHEN J. O'BRIEN, NIH/NCI  
STEPHEN HARRIS, Oxford University -  
Genetic Diversity in Semi-Arid Tree  
Legumes  
**Wine & Cheese Reception**

#### TUESDAY, JANUARY 16

##### Continental Breakfast

##### Session 3 - Hosts, Pathogens and Diseases

Chairperson GARY TOENNIENSEN,  
The Rockefeller Foundation

##### Plenary Lecture -

BRIAN STASKAWICZ, UC Berkeley

SALLY A. LEONG, USDA PDRRU -

The avrC039 Locus of Rice Blast

Fungus Magnaporthe Grisea

JAN LEACH, Kansas State Univ

##### Posters (even #'s) Exhibits & Computer Demos - Coffee/Soda

##### Afternoon - Computer Tools & Resources

Chairperson MICHAEL CHERRY,  
Stanford University

##### Workshops

IGGI: Michael Gale/Calvin Quaslet/ Jeff  
Bennetzen

Abiotic Stress: Henry Nguyen

#### WEDNESDAY, JANUARY 17

##### Continental Breakfast

##### Session 4 - Comparative Mapping

Chairperson Mark Sorrells, Cornell  
Univ.

##### Plenary Lecture -

RONALD PHILLIPS, Univ. of Minnesota -  
Extensions of Comparative Mapping

JEAN CHRISTOPHE GLASZMANN,  
CIRAD

The Genome of Modern Sugarcane

Cultivars

DEREK LYDiate, JIC

JOHN HESLOP-HARRISON,

Comparative Analysis of Plant Genome

Architecture

##### Session 5 - Gene and Chromosome Organization

Chairperson  
BRIAN LARKINS, University of Arizona

Molecular Genetic Approaches for  
Developing Quality Protein Maize  
ELIZABETH BLACKBURN, UC San  
Francisco

Telomeres and Telomerases

MARGORIE MATZKE, Austrian

Academy of Sciences, Vienna

Homology-Dependent Gene Silencing in

Transgenic Tobacco Plants

##### Posters (odd #'s) Exhibits & Computer Demos

##### Workshops

Nomenclature: Carl Price/Ellen

Reardon

ITMI: Michael Gale/Jeff Bennetzen

Fruit Tree: Norman Weeden

Barley: Patrick Hayes

##### Conference Dinner

#### THURSDAY, JANUARY 18

##### Continental Breakfast

##### Session #6 - Applications of Molecular Markers in Breeding

Chairperson CHARLES STUBER, USDA

##### Plenary Lecture -

CAROLINE O'NEILL, CNN

DANNY ALEXANDER, Ciba-Geigy

Marker Assisted Maize Breeding in the  
Real World

REBECCA NELSON

##### Posters (even #'s) Exhibits & Computer Demos

JOHN SNAPE, JIC

DAVID HOISINGTON, CIMMYT

International

Application of Molecular Markers for

Improving Drought and Insect

Resistance in Tropical Maize

MARTIN GANAL, IPK

Isolation and Characterization of

Wheat Microsatellite Markers

STEPHEN HELLER, USDA/ARS and

JEROME MIKSCHKE, USDA/ARS -

Closing Remarks

## Plant Genome IV



#### Registration Fees:

- ☐ \$375 On-Site Registration (Postmarked after November 15)
- ☐ \$325 Pre-Registration (Postmarked between October 17 & November 15)
- ☐ \$300 Pre-Registration (Postmarked by October 16)
- ☐ \$100 Student Registration (Student Rate does not apply to Postdoctoral applicants)

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Affiliation/Department

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City  State  Zip

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Make checks payable to: Scherago International, Inc /Plant Genome

## Plant Genome Publications

The following publications are available. If you would like to receive a copy, check off the title and mail your request to:

Plant Genome Data and Information Center  
National Agricultural Library, ARS, USDA  
10301 Baltimore Blvd., 4th Floor  
Beltsville, MD 20705-2351

### CRIS/ICAR Projects and Bibliographies:

The sponsored research projects were obtained by searching CRIS/ICAR (USDA and CARC, North America) using AGRISEARCH Silver Platter CD. Bibliographies were obtained by searching AGRICOLA Silver Platter CD.

Gene Expression in Cereal Crops. June 1992 - May 1994. (QB94-57)

Herbicide Tolerance/Resistance in Plants. April 1992 - March 1994. (QB94-60)

Tomato and Potato Genome Mapping. February 1994. Compiled by Andrew Kalinski.

Transgenic Rice. January 1994. Compiled by Andrew Kalinski.

Transgenic Tomato. February 1994. Compiled by Andrew Kalinski.

Wheat, Barley, Rice, Rye, and Oat Genome Mapping. January 1994. Compiled by Andrew Kalinski.

### INTERNET Resources:

A Biologist's Guide to Internet Resources, version 1.7 (November 1993) and 1.8a. Una Smith. December 1994.

A Guide to Environmental Resources on the Internet. December 1994.

A Guide to Internet/Bitnet Resources in Agriculture and Related Sciences. June 1994.

Entering the World-Wide Web: A Guide to Cyberspace. Kevin Hughes. October 1993.

Federal Government Information on Internet. July 1994.

List of Molecular Biology E-mail Servers. Prepared by Amos Bairoch, Dept of Medical Biochemistry, University of Switzerland.

### Other Informational Products:

Prepared by the Genome Informatics Group.

Plant Genome Database CD-ROM



Plant Genome Data  
and Information Center  
USDA - ARS - NAL  
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Beltsville, Maryland 20705-2351

ISSN: 1057-2600

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